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Sequence Listing could not be accepted due to errors.
See attached Validation Report.
If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).
Reviewer: Durreshwar Anjum
Timestamp: [year=2008; month=12; day=17; hr=13; min=47; sec=20; ms=268;
]
================================================================



****************************************************************
Reviewer Comments:
<220>
<221>  Xaa
<222>  (11)..(11)
<223>  Xaa is a single amino acid that can be either Met, Ile, or Val.



<400>  3

Phe Xaa Pro Xaa Xaa Xaa Tyr Xaa Xaa Xaa Xaa Xaa Xaa Pro Xaa Asp
1               5                   10                  15


Missing explanation for 'Xaa' at location 15.  Please check for similar
errors in subsequent sequences.

<210>  7
<211>  110
<212>  PRT
<213>  Homo sapiens, bromodomain peptide

<400>  7
Numeric identifier <213> can only be one of three choices, "Scientific
name, i.e. Genus/species, Unknown or Artificial Sequence." For all
sequences using "Unknown or Artificial sequence", for numeric identifier
<213>, a mandatory feature is required to explain the source of the
genetic material. The feature consists of <220>, which remains blank,
and <223>, which states the source of the genetic material. To explain
the source, if the sequence is put together from several organisms,
please list those organisms. If the sequence is made in the laboratory,
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please indicate that the sequence is synthesized. Please make all necessary changes, if similar errors detected in subsequent sequences.

* *

Application No: 09510314   Version No: 3.0

Input Set:

Output Set:

Started:	2008-12-02 17:33:31.534
Finished:	2008-12-02 17:33:35.791
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Total Errors:	23
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        Input Set:


        Output Set:



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       Finished:    2008-12-02 17:33:35.791
        Elapsed:    0 hr(s) 0 min(s) 4 sec(s) 257 ms
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No. of SeqIDs Defined:    44
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E 321	No. of Bases conflict, this line has no nucleotides SEQID (44)

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<110>   Zhou, Ming-Ming
        Aggarwal, Aneel

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<212>   PRT
<213>   Homo sapiens

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        35                  40                  45


Ser Gly Ala Cys Gly Pro Ala Thr Ala Val Ala Ala Ala Gly Thr Ala
    50                  55                  60


Glu Gly Pro Gly Gly Gly Gly Ser Ala Arg Ile Ala Val Lys Lys Ala
65                  70                  75                  80


Gln Leu Arg Ser Ala Pro Arg Ala Lys Lys Leu Glu Lys Leu Gly Val
                85                  90                  95


Tyr Ser Ala Cys Lys Ala Glu Glu Ser Cys Lys Cys Asn Gly Trp Lys
                100                 105                 110


Asn Pro Asn Pro Ser Pro Thr Pro Pro Arg Ala Asp Leu Gln Gln Ile
            115                 120                 125


Ile Val Ser Leu Thr Glu Ser Cys Arg Ser Cys Ser His Ala Leu Ala
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Ala His Val Ser His Leu Glu Asn Val Ser Glu Glu Glu Met Asn Arg
145                 150                 155                 160
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Leu Leu Gly Ile Val Leu Asp Val Glu Tyr Leu Phe Thr Cys Val His
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Lys Glu Glu Asp Ala Asp Thr Lys Gln Val Tyr Phe Tyr Leu Phe Lys
            180   185   190

Leu Leu Arg Lys Ser Ile Leu Gln Arg Gly Lys Pro Val Val Glu Gly
            195   200   205

Ser Leu Glu Lys Lys Pro Pro Phe Glu Lys Pro Ser Ile Glu Gln Gly
            210   215   220

Val Asn Asn Phe Val Gln Tyr Lys Phe Ser His Leu Pro Ala Lys Glu
225   230   235   240

Arg Gln Thr Ile Val Glu Leu Ala Lys Met Phe Leu Asn Arg Ile Asn
            245   250   255

Tyr Trp His Leu Glu Ala Pro Ser Gln Arg Arg Leu Arg Ser Pro Asn
            260   265   270

Asp Asp Ile Ser Gly Tyr Lys Glu Asn Tyr Thr Arg Trp Leu Cys Tyr
            275   280   285

Cys Asn Val Pro Gln Phe Cys Asp Ser Leu Pro Arg Tyr Glu Thr Thr
            290   295   300

Gln Val Phe Gly Arg Thr Leu Leu Arg Ser Val Phe Thr Val Met Arg
305   310   315   320

Arg Gln Leu Leu Glu Gln Ala Arg Gln Glu Lys Asp Lys Leu Pro Leu
            325   330   335

Glu Lys Arg Thr Leu Ile Leu Thr His Phe Pro Lys Phe Leu Ser Met
            340   345   350

Leu Glu Glu Glu Val Tyr Ser Gln Asn Ser Pro Ile Trp Asp Gln Asp
            355   360   365

Phe Leu Ser Ala Ser Ser Arg Thr Ser Gln Leu Gly Ile Gln Thr Val
            370   375   380

Ile Asn Pro Pro Pro Val Ala Gly Thr Ile Ser Tyr Asn Ser Thr Ser
385   390   395   400

Ser Ser Leu Glu Gln Pro Asn Ala Gly Ser Ser Ser Pro Ala Cys Lys
            405   410   415

Ala Ser Ser Gly Leu Glu Ala Asn Pro Gly Glu Lys Arg Lys Met Thr
            420   425   430

Asp Ser His Val Leu Glu Glu Ala Lys Lys Pro Arg Val Met Gly Asp
            435   440   445

Ile Pro Met Glu Leu Ile Asn Glu Val Met Ser Thr Ile Thr Asp Pro
            450   455   460

Ala Ala Met Leu Gly Pro Glu Thr Asn Phe Leu Ser Ala His Ser Ala
465   470   475   480

Arg Asp Glu Ala Ala Arg Leu Glu Glu Arg Arg Gly Val Ile Glu Phe
                485   490   495

His Val Val Gly Asn Ser Leu Asn Gln Lys Pro Asn Lys Lys Ile Leu
                500   505   510

Met Trp Leu Val Gly Leu Gln Asn Val Phe Ser His Gln Leu Pro Arg
        515   520   525

Met Pro Lys Glu Tyr Ile Thr Arg Leu Val Phe Asp Pro Lys His Lys
        530   535   540

Thr Leu Ala Leu Ile Lys Asp Gly Arg Val Ile Gly Gly Ile Cys Phe
545   550   555   560

Arg Met Phe Pro Ser Gln Gly Phe Thr Glu Ile Val Phe Cys Ala Val
                565   570   575

Thr Ser Asn Glu Gln Val Lys Gly Tyr Gly Thr His Leu Met Asn His
                580   585   590

Leu Lys Glu Tyr His Ile Lys His Asp Ile Leu Asn Phe Leu Thr Tyr
        595   600   605

Ala Asp Glu Tyr Ala Ile Gly Tyr Phe Lys Lys Gln Gly Phe Ser Lys
        610   615   620

Glu Ile Lys Ile Pro Lys Thr Lys Tyr Val Gly Tyr Ile Lys Asp Tyr
625   630   635   640

Glu Gly Ala Thr Leu Met Gly Cys Glu Leu Asn Pro Arg Ile Pro Tyr
                645   650   655

Thr Glu Phe Ser Val Ile Ile Lys Lys Gln Lys Glu Ile Ile Lys Lys
                660   665   670

Leu Ile Glu Arg Lys Gln Ala Gln Ile Arg Lys Val Tyr Pro Gly Leu
        675   680   685

Ser Cys Phe Lys Asp Gly Val Arg Gln Ile Pro Ile Glu Ser Ile Pro
        690   695   700

Gly Ile Arg Glu Thr Gly Trp Lys Pro Ser Gly Lys Glu Lys Ser Lys
705   710   715   720

Glu Pro Arg Asp Pro Asp Gln Leu Tyr Ser Thr Leu Lys Ser Ile Leu
                725   730   735

Gln Gln Val Lys Ser His Gln Ser Ala Trp Pro Phe Met Glu Pro Val
                740   745   750

Lys Arg Thr Glu Ala Pro Gly Tyr Tyr Glu Val Ile Arg Phe Pro Met
        755   760   765

Asp Leu Lys Thr Met Ser Glu Arg Leu Lys Asn Arg Tyr Tyr Val Ser
    770   775   780

Lys Lys Leu Phe Met Ala Asp Leu Gln Arg Val Phe Thr Asn Cys Lys
785   790   795   800

Glu Tyr Asn Ala Ala Glu Ser Glu Tyr Tyr Lys Cys Ala Asn Ile Leu
                805   810   815

Glu Lys Phe Phe Phe Ser Lys Ile Lys Glu Ala Gly Leu Ile Asp Lys
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<213> Artificial Sequence

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<223> synthetic bromodomain peptide

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<222> (2)..(4)
<223> Xaa is a maximum of three amino acids. Each of these can be any amino acid. One may be missing.

<220>
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<223> Xaa is a maximum of eight amino acids. Each of these can be any amino acid. One, two, or three may be missing.

<220>
<221> Xaa
<222> (5)..(5)
<223> Xaa is a single amino acid that is either Pro, Lys, or His.

<220>
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<222> (6)..(6)
<223> Xaa is any single amino acid.

<220>
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<222> (8)..(8)
<223> Xaa is a single amino acid that can be either Tyr, Phe, or His.

<220>
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<222> (9)..(13)

<223> Xaa is 5 amino acids. Each of these can be any amino acid.

<220>
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<223> Xaa is a single amino acid that can be either Met, Ile, or Val.

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1   5   10   15

<210> 4
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<223> Xaa represents an acetyl-lysine

<400> 4

Ile Ser Tyr Gly Arg Xaa Lys Arg Arg Gln Arg Arg
1   5   10

<210> 5
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<220>
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<223> Xaa represents an acetyl lysine.

<400> 5

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1   5   10

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Gln Ser Thr Ser Arg His Lys Xaa Leu Met Phe Lys Thr Glu
1   5   10

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Ser Lys Glu Pro Arg Asp Pro Asp Gln Leu Tyr Ser Thr Leu Lys Ser
1   5   10   15

Ile Leu Gln Gln Val Lys Ser His Gln Ser Ala Trp Pro Phe Met Glu
            20   25   30

Pro Val Lys Arg Thr Glu Ala Pro Gly Tyr Tyr Glu Val Ile Arg Ser
            35   40   45

Pro Met Asp Leu Lys Thr Met Ser Glu Arg Leu Lys Asn Arg Tyr Tyr
    50   55   60

Val Ser Lys Lys Leu Phe Met Ala Asp Leu Gln Arg Val Phe Thr Asn
65   70   75   80

Cys Lys Glu Tyr Asn Ala Pro Glu Ser Glu Tyr Tyr Lys Cys Ala Asn
                85   90   95

Ile Leu Glu Lys Phe Phe Phe Ser Lys Ile Lys Glu Ala Gly
            100   105   110

<210> 8
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<212> PRT
<213> Homo sapiens

<400> 8

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1   5   10   15

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            20   25   30

Pro Val Lys Lys Ser Glu Ala Pro Asp Tyr Tyr Glu Val Ile Arg Phe
        35   40   45

Pro Ile Asp Leu Lys Thr Met Thr Glu Arg Leu Arg Ser Arg Tyr Tyr
        50   55   60

Val Thr Arg Lys Leu Phe Val Ala Asp Leu Gln Arg Val Ile Ala Asn
65   70   75   80

Cys Arg Glu Tyr Asn Pro Pro Asp Ser Glu Tyr Cys Arg Cys Ala Ser
                85   90   95

Ala Leu Glu Lys Phe Phe Tyr Phe Lys Leu Lys Glu Gly Gly
            100   105   110

<210>   9
<211>   109
<212>   PRT
<213>   Tetrahymena thermophila

<400>   9

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1   5   10   15

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                20   25   30

Val Asn Lys Asp Asp Val Pro Asp Tyr Tyr Asp Val Ile Thr Asp Pro
            35   40   45

Ile Asp Ile Lys Ala Ile Glu Lys Lys Leu Gln Asn Asn Gln Tyr Val
        50   55   60

Asp Lys Asp Gln Phe Ile Lys Asp Val Lys Arg Ile Phe Thr Asn Ala
65   70   75   80

Lys Ile Tyr Asn Gln Pro Asp Thr Ile Tyr Tyr Lys Ala Ala Lys Glu
                85   90   95

Leu Glu Asp Phe Val Glu Pro Tyr Leu Thr Lys Leu Lys
            100   105

<210>   10
<211>   109
<212>   PRT
<213>   Saccharomyces cerevisiae

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Ala Gln Arg Pro Lys Arg Gly Pro His Asp Ala Ala Ile Gln Asn Ile
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Val Asn Lys Glu Glu Val Pro Asp Tyr Tyr Asp Phe Ile Lys Glu Pro
        35   40   45

Met Asp Leu Ser Thr Met Glu Ile Lys Leu Glu Ser Asn Lys Tyr Gln
        50   55   60

Lys Met Glu Asp Phe Ile Tyr Asp Ala Arg Leu Val Phe Asn Asn Cys
65   70   75   80

Arg Met Tyr Asn Gly Glu Asn Thr Ser Tyr Tyr Lys Tyr Ala Asn Arg
                85   90   95

Leu Glu Lys Phe Phe Asn Asn Lys Val Lys Glu Ile Pro
                100   105

<210>   11
<211>   112
<212>   PRT
<213>   Homo sapiens

<400>   11

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1   5   10   15

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                20   25   30

Pro Val Asp Pro Gln Leu Leu Gly Ile Pro Asp Tyr